

SEQUENCE LISTING

<110> Gilbert, Teresa
 Hart, Charles E.
 Sheppard, Paul O.
 Gilbertson, Debra G.

<120> GROWTH FACTOR HOMOLOG ZVEGF4

<130> 99-19

<150> US 60/132,250

<151> 1999-05-03

<150> US 60/164,463

<151> 1999-11-10

<150> US 60/180,169

<151> 2000-02-04

<160> 53

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1882

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (226)...(1338)

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cagggcgagc gcaggcggcg agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac	180
ccggcctttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc	237
Met His Arg Leu	

atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac	285
Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp	
5 10 15 20	
act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc	333
Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala	
25 30 35	
aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga	381
Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg	
40 45 50	
gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga	429
Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg	
55 60 65	
ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac	477
Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His	
70 75 80	
tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga	525
Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly	
85 90 95 100	
tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt	573
Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val	
105 110 115	
gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga	621
Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly	
120 125 130	
cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa	669
His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys	
135 140 145	
atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag	717
Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys	
150 155 160	
att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag	765
Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu	
165 170 175 180	

acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac	813
Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn	
185 190 195	
tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa	861
Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys	
200 205 210	
aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat	909
Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn	
215 220 225	
cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct	957
Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro	
230 235 240	
cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg	1005
Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu	
245 250 255 260	
gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat	1053
Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn	
265 270 275	
tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc	1101
Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe	
280 285 290	
ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt	1149
Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys	
295 300 305	
gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg	1197
Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val	
310 315 320	
aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg	1245
Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg	
325 330 335 340	

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
 345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg agggtgagat 1398
 aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
 agtggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca 1518
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 ataaatttat ttttaaattt tgaaacacga aacaattttg aatcttgctc tcttaaagaa 1818
 agcatcttgt atattaaaaa tcaaaagatg aggctttctt acatatacat cttagttgat 1878
 tatt 1882

<210> 2

<211> 370

<212> PRT

<213> Homo sapiens

<400> 2

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
 1 5 10 15
 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
 20 25 30
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
 35 40 45
 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
 50 55 60
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65 70 75 80
 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
 85 90 95
 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
 115 120 125
 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 130 135 140

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
 180 185 190
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
 195 200 205
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 225 230 235 240
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 275 280 285
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 3

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide motif

<221> VARIANT

<222> (2)...(19)

<223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (20)...(34)
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT
 <222> (36)...(45)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (46)...(72)
 <223> Xaa = Any Amino Acid or is not present

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 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (94)...(123)
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT
 <222> (125)...(125)
 <223> Xaa = Any Amino Acid

<400> 3

Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		20					25					30			
Xaa	Xaa	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40					45			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50				55				60					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70				75					80	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			85					90						95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105						110	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys		
		115						120					125		

<210> 4

<211> 24
 <212> PRT
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<220>
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<221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Lys or Arg

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Asp, Asn or Glu

<221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Trp, Tyr or Phe

<221> VARIANT
 <222> (6)...(16)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (17)...(20)
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT
 <222> (22)...(22)
 <223> Xaa = Lys or Arg

<221> VARIANT
 <222> (23)...(23)
 <223> Xaa = Trp, Tyr or Phe

<400> 4
 Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Gly Xaa Xaa Cys
 20

<210> 5
 <211> 6

<212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide tag

<400> 5
 Glu Tyr Met Pro Met Glu
 1 5

<210> 6
 <211> 1110
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> degenerate sequence

<221> misc_feature
 <222> (1)...(1110)
 <223> n = A,T,C or G

<400> 6
 atgcaymgny tnathttygt ntayacnytn athtgygcna aytttygyws ntgymgngay 60
 acnwsngcna cncncarws ngcnwsnath aargcnytnm gnaaygcnaa yytnmgnmgn 120
 gaygarwsna aycayytnac ngayytnay mgnmngayg aracnathca rgtnaarggn 180
 aayggntayg tncarwsncc nmgnnttyccn aaywsntayc cnmgnaayt nytnytnacn 240
 tggmgnytn c aywsncarga raayacnmgn athcarytng tnttygayaa ycarttyggn 300
 ytnngargarg cngaraayga yathtgymgn taygayttyg tngargtnga rgayathwsn 360
 garacnwsna cnathathmg nggnmgntgg tgyggncaya argargtncc nccnmgnath 420
 aarwsnmgna cnaaycarat haarathacn ttyaarwsng aygaytaytt ygtngcnaar 480
 ccnggnttya arathtayta ywsnytnytn gargayttyc arccngcngc ngcnwsngar 540
 acnaaytggg arwsngtnac nwsnwsnath wsngngtnw sntayaayws nccnwsngtn 600
 acngayccna cnytnathgc ngaygcnytn gayaaraara thgcngartt ygayacngtn 660
 gargayytny tnaartaytt yaayccngar wsntggcarg argayytnga raayatgtay 720
 ytngayacnc cnmgntaymg nggnmgnwsn taycaygaym gnaarwsnaa rgtngayytn 780
 gaymgnytna aygaygayc naarmgntay wsntgyacnc cnmgnaayta ywsngtnaay 840
 athmgngarg arytnaaryt ngcnaaygtn gtnttyttyc cnmgntgyt nytngtncar 900
 mgntgyggng gnaaytgygg ntgyggnacn gtnaaytggm gnwsntgyac ntgyaaywsn 960
 ggnaaracng tnaaraarta ycaygargtn ytncarttyg arccnggnca yathaarmgn 1020
 mgnggnmgng cnaaracnat ggcnytngtngn gayathcary tngaycayca ygarmgntgy 1080
 gaytgyatht gywsnwsnmg nccnccnmgn 1110

<210> 7
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 7
 mgntgyggng gnaaytg

17

<210> 8
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 8
 mgntgydsng gnwrytg

17

<210> 9
 <211> 17
 <212> DNA
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<220>
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<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 9

carywnccns hrcanck

17

<210> 10

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 10

ttyttyccnm gntgyyt

17

<210> 11

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 11

ntnddnccnn sntgybt

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<210> 12

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

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avrcansnng gnhnna	17
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<222> (1)...(17)	
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<400> 13	
caygarmgnt gygaytg	17
<210> 14	
<211> 17	
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caynnnnvnt gyvvntg	17
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<222> (1)...(17)

<223> n = A,T,C or G

<400> 15

canbbrcanb nnnnrtg

17

<210> 16

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 16

tgyacnccnm gnaayta

17

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 17

tgyhnnmcmn knrmdh

17

<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 18
 dhnkynmkng knndrca 17

<210> 19
 <211> 18
 <212> DNA
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<220>
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<221> misc_feature
 <222> (1)...(18)
 <223> n = A,T,C or G

<400> 19
 ntaygaytwy gtngargt 18

<210> 20
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(18)
 <223> n = A,T,C or G

<400> 20
 natrcdrawr canctyca 18

<210> 21
 <211> 18
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<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(18)

<223> n = A,T,C or G

<400> 21

gntdbccnma ndvntayc

18

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(18)

<223> n = A,T,C or G

<400> 22

cnahvggnkt nhbnatrg

18

<210> 23

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(18)

<223> n = A,T,C or G

<400> 23

tnhdnggnmr ntdbtgyg

18

<210> 24

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(18)

<223> n = A,T,C or G

<400> 24

andhnccnky nahvacrc

18

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC21,119

<400> 25

aggacgatgg tgtggacaca agga

24

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC21,120

<400> 26

tccagagcat ccgcaatcag agtg

24

<210> 27

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer ZC21,987

<400> 27

caacctgttg tttgtcccgt cacc

24

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17,251

<400> 28

tctggacgtc ctctgctgg tatag

25

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17,252

<400> 29

ggtatggagc aaggggcaag ttggg

25

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17,156

<400> 30

gagtggcaac ttccagggcc aggagag

27

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer ZC17,157

<400> 31
cttttgctag cctcaaccct gactatc 27

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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (154)...(1191)

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attatgtgga aactaccctg cgattctctg ctgccagagc aggctcggcg cttccacccc 60
agtgcagcct tcccctggcg gtggtgaaag agactcggga gtcgctgctt ccaaagtgcc 120
cgccgtgagt gagctctcac cccagtcagc caa atg agc ctc ttc ggg ctt ctc 174
Met Ser Leu Phe Gly Leu Leu
1 5
ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa 222
Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu
10 15 20
tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac 270
Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn
25 30 35
gga gta caa gat cct cag cat gag aga att att act gtg tct act aat 318
Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn
40 45 50 55
gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg 366
Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr
60 65 70
gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa 414
Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln
75 80 85
ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata 462
Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile
90 95 100

tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata	510
Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile	
105 110 115	
tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct	558
Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser	
120 125 130 135	
aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct	606
Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro	
140 145 150	
tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc	654
Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe	
155 160 165	
aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg	702
Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu	
170 175 180	
gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt	750
Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu	
185 190 195	
att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta	798
Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu	
200 205 210 215	
tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga	846
Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg	
220 225 230	
aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta	894
Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu	
235 240 245	
tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta	942
Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu	
250 255 260	
aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc	990
Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg	
265 270 275	

tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa 1038
 Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln
 280 285 290 295

tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg 1086
 Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu
 300 305 310

aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg 1134
 Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val
 315 320 325

gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca 1182
 Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr
 330 335 340

gga gga tag ccgcatcacc accagcagct cttgccaga gctgtgcagt 1231
 Gly Gly *
 345

gcagtggctg attctattag agaacgtatg cgttatctcc atccttaatc tcagttgttt 1291
 gcttcaagga cttttcatct tcaggattta cagtgcattc tgaaagagga gacatcaaac 1351
 agaattagga gttgtgcaac agctcttttg agaggaggcc taaaggacag gagaaaagg 1411
 cttcaatcgt ggaaagaaaa tttaatgttg tattaaatag atcaccagct agtttcagag 1471
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 ggtaatgtca gtacagggaaa aaaactgtgc aagtgagcac ctgattccgt tgccttgctt 1591
 aactctaaag ctccatgtcc tgggcctaaa atcgtataaa atctggattt ttttttttt 1651
 tttttgctca tattcacata tgtaaacag aacattctat gtactacaaa cctgggtttt 1711
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<210> 33

<211> 345

<212> PRT

<213> Homo sapiens

<400> 33

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 Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
 35 40 45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
 50 55 60
 His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
 65 70 75 80
 Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
 85 90 95
 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
 100 105 110
 Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
 115 120 125
 Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
 130 135 140
 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
 145 150 155 160
 Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
 165 170 175
 Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
 180 185 190
 Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
 195 200 205
 Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
 210 215 220
 Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
 225 230 235 240
 Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
 245 250 255
 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
 260 265 270
 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
 275 280 285
 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
 290 295 300
 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
 305 310 315 320
 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
 325 330 335
 Cys Val Cys Arg Gly Ser Thr Gly Gly
 340 345

<210> 34

<211> 3571

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1049)...(2086)

<400> 34

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ctgcccagc acctgttggc ccgcccagctg gccgcccgcg ccccccgcgc ccccccgcgc    180
cgcccggccg ccagccccgc gcccgcgcg ccgcccgtg ggggaaagt gagacgggga    240
ggggacaaga gcgacccctc aggccagcca ggccttcct tagccgcccg tgcttagccg    300
ccacctctcc tcagccctgc gtccctgcct gccttagggc aggcattcca gcgctcgcga    360
ctccgagccg cccaagctct cccggcttcc cgcagcactt cgccggtacc cgagggaaact    420
tcggtggcca ccgactgcag caaggaggag gtcgcgcggt ggatccgggc cagtcccag    480
tcgtccccgc ggccctctct cccgcccggg accgcgcg cactcgcagg gcacggtccc    540
ctccccccag gtgggggttg ggcgcccgcct gccgcccga tcagcagctt tgcattgat    600
cccaagggtc tcgcctcgt gccgacctg cttccagtct ggcttggcg gaccccgagt    660
cctcgctgt gtccgtgcc ccaaactgac aggtgctccc tgcgagtcgc cagactcat    720
cgccgctccc ccgcgtcccc accccttctt tctccctcg cctaccccca ccccccgcac    780
ttcggcacag ctcaggattt gtttaaact tgggaaact gttcaggctc aggttttgc    840
ttgatccttt tcaaaaact gagacacaga agagggtctt aggaaaaact tttgatggg    900
attatgtgga aactaccctg cgattctct ctgccagagc cggccaggcg cttccaccgc    960
agcgcagcct ttccccggc gggctgagcc ttggagtcgt cgcttcccca gtgcccgcg    1020
cgagtgagcc ctgccccag tcagccaa atg ctc ctc ctc ggc ctc ctc ctg    1072

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Met Leu Leu Leu Gly Leu Leu Leu

1

5

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ctg aca tct gcc ctg gcc ggc caa aga acg ggg act cgg gct gag tcc    1120
Leu Thr Ser Ala Leu Ala Gly Gln Arg Thr Gly Thr Arg Ala Glu Ser
10 15 20

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aac ctg agc agc aag ttg cag ctc tcc agc gac aag gaa cag aac gga    1168
Asn Leu Ser Ser Lys Leu Gln Leu Ser Ser Asp Lys Glu Gln Asn Gly
25 30 35 40

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gtg caa gat ccc cgg cat gag aga gtt gtc act ata tct ggt aat ggg    1216
Val Gln Asp Pro Arg His Glu Arg Val Val Thr Ile Ser Gly Asn Gly
45 50 55

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agc atc cac agc ccg aag ttt cct cat aca tac cca aga aat atg gtg    1264
Ser Ile His Ser Pro Lys Phe Pro His Thr Tyr Pro Arg Asn Met Val
60 65 70

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ctg gtg tgg aga tta gtt gca gta gat gaa aat gtg cgg atc cag ctg	1312
Leu Val Trp Arg Leu Val Ala Val Asp Glu Asn Val Arg Ile Gln Leu	
75 80 85	
aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc	1360
Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys	
90 95 100	
aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta	1408
Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu	
105 110 115 120	
gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa	1456
Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys	
125 130 135	
gga aat cat atc agg ata aga ttt gta tct gat gag tat ttt cca tct	1504
Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser	
140 145 150	
gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca	1552
Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr	
155 160 165	
gaa acc acg agt cct tcg gtg ttg ccc cct tca tct ttg tca ttg gac	1600
Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp	
170 175 180	
ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att	1648
Leu Leu Asn Asn Ala Val Thr Ala Phe Ser Thr Leu Glu Glu Leu Ile	
185 190 195 200	
cgg tac cta gag cca gat cga tgg cag gtg gac ttg gac agc ctc tac	1696
Arg Tyr Leu Glu Pro Asp Arg Trp Gln Val Asp Leu Asp Ser Leu Tyr	
205 210 215	
aag cca aca tgg cag ctt ttg ggc aag gct ttc ctg tat ggg aaa aaa	1744
Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys	
220 225 230	
agc aaa gtg gtg aat ctg aat ctc ctc aag gaa gag gta aaa ctc tac	1792
Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr	
235 240 245	

agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag 1840
 Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys
 250 255 260

agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt 1888
 Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys
 265 270 275 280

gga gga aat tgt gcc tgt tgt ctc cat aat tgc aat gaa tgt cag tgt 1936
 Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys
 285 290 295

gtc cca cgt aaa gtt aca aaa aag tac cat gag gtc ctt cag ttg aga 1984
 Val Pro Arg Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg
 300 305 310

cca aaa act gga gtc aag gga ttg cat aag tca ctc act gat gtg gct 2032
 Pro Lys Thr Gly Val Lys Gly Leu His Lys Ser Leu Thr Asp Val Ala
 315 320 325

ctg gaa cac cac gag gaa tgt gac tgt gtg tgt aga gga aac gca gga 2080
 Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Asn Ala Gly
 330 335 340

ggg taa ctgcagcctt cgtagcagca cacgtgagca ctggcattct gtgtaccccc 2136
 Gly *
 345

acaagcaacc ttcatcccca ccagcggttg ccgcagggt ctcagctgct gatgctggct 2196
 atggtaaaga tcttactcgt ctccaaccaa attctcagtt gtttgcttca atagccttcc 2256
 cctgcaggac ttcaagtgtc ttctaaaaga ccagaggcac caagaggagt caatcacaaa 2316
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 aatgtagatc gctagcaaac tctggagtga cagcatttct tttccactga cagaatgggtg 2436
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<210> 35

<211> 345

<212> PRT

<213> Mus musculus

<400> 35

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 Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
 35 40 45
 Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
 50 55 60
 His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
 65 70 75 80
 Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
 85 90 95
 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
 100 105 110
 Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
 115 120 125
 Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
 130 135 140
 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
 145 150 155 160
 Ser Ile Ile Met Pro Gln Val Thr Glu Thr Thr Ser Pro Ser Val Leu
 165 170 175
 Pro Pro Ser Ser Leu Ser Leu Asp Leu Leu Asn Asn Ala Val Thr Ala
 180 185 190
 Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
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<210> 36
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (496)...(592)
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gcctctcagg	ggccgcggcc	ggggctggag	aacgctgctg	ctccgctcgc	ctgccccgct					180
agattcggcg	ctgcccggcc	cctgcagcct	gtgctgcagc	tgccggccac	cggagggggc					240
gaacaaacaa	acgtcaacct	gttgtttgtc	ccgtcaccat	ttatcagctc	agcaccacaa					300
ggaagtgcgg	caccacacg	cgctcgaaa	gttcagcatg	caggaagttt	gggagagct					360
cggcgattag	cacagcgacc	cgggccagcg	cagggcgagc	gcagacggcg	agagcgcagg					420
gcggcgcggc	gtcgttcccg	ggagcagaac	ccggcttttt	cttgagcgga	cgctgtctct					480
agtcgctgat	cccaa atg	cac cgg ctc	atc ttt gtc	tac act cta	atc tgc					531
	Met His	Arg Leu	Ile Phe	Val Tyr	Thr Leu	Ile Cys				
	1		5		10					

gca aac ttt tgc agc tgt cgg gac act tct gca acc ccg cag agc gca 579
 Ala Asn Phe Cys Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala
 15 20 25

tcc atc aaa gct t gagtattc 600
 Ser Ile Lys Ala
 30

<210> 37

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC22,685

<400> 37

gccgtcacca tttatcag 18

<210> 38

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC22,686

<400> 38

cggtcgctg tgctaadc 18

<210> 39

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 39

Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln
 1 5 10 15
 Ile Lys

<210> 40
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide

<400> 40
 Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg
 1 5 10 15
 Tyr Arg Gly Arg Ser Tyr His Asp Cys
 20 25

<210> 41
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide

<400> 41
 Cys Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met
 1 5 10 15
 Ala Leu Val Asp Ile Gln Leu Asp
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<210> 42
 <211> 6
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 <213> Artificial Sequence

<220>
 <223> peptide

<400> 42
 Glu Tyr Met Pro Thr Asp
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<210> 43

<211> 42
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<220>
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<400> 43
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<210> 44
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<220>
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<400> 44
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 <223> oligonucleotide primer ZC22342

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<400> 47
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<210> 48
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<220>
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<400> 48
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<210> 49
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 <212> DNA
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<220>
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<400> 49
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<210> 50
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<220>
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<400> 50
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<210> 51
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 <212> DNA
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<220>
 <223> oligonucleotide primer ZC14063

<400> 51
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<210> 52
 <211> 1472
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (93)...(1205)

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 gagcaacgcg atccctaggt cgctgagccc aa atg caa cgg ctc gtt tta gtc 113
 Met Gln Arg Leu Val Leu Val
 1 5
 tcc att ctc ctg tgc gcg aac ttt agc tgc tat ccg gac act ttt gcg 161
 Ser Ile Leu Leu Cys Ala Asn Phe Ser Cys Tyr Pro Asp Thr Phe Ala
 10 15 20
 act ccg cag aga gca tcc atc aaa gct ttg cgc aat gcc aac ctc agg 209
 Thr Pro Gln Arg Ala Ser Ile Lys Ala Leu Arg Asn Ala Asn Leu Arg
 25 30 35
 aga gat gag agc aat cac ctc aca gac ttg tac cag aga gag gag aac 257
 Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Gln Arg Glu Glu Asn
 40 45 50 55
 att cag gtg aca agc aat ggc cat gtg cag agt cct cgc ttc ccg aac 305
 Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro Asn
 60 65 70

agc tac cca agg aac ctg ctt ctg aca tgg tgg ctc cgt tcc cag gag	353
Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln Glu	
75 80 85	
aaa aca cgg ata caa ctg tcc ttt gac cat caa ttc gga cta gag gaa	401
Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu Glu	
90 95 100	
gca gaa aat gac att tgt agg tat gac ttt gtg gaa gtt gaa gaa gtc	449
Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Glu Val	
105 110 115	
tca gag agc agc act gtt gtc aga gga aga tgg tgt ggc cac aag gag	497
Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys Glu	
120 125 130 135	
atc cct cca agg ata acg tca aga aca aac cag att aaa atc aca ttt	545
Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr Phe	
140 145 150	
aag tct gat gac tac ttt gtg gca aaa cct gga ttc aag att tat tat	593
Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr Tyr	
155 160 165	
tca ttt gtg gaa gat ttc caa ccg gaa gca gcc tca gag acc aac tgg	641
Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn Trp	
170 175 180	
gaa tca gtc aca agc tct ttc tct ggg gtg tcc tat cac tct cca tca	689
Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro Ser	
185 190 195	
ata acg gac ccc act ctc act gct gat gcc ctg gac aaa act gtc gca	737
Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val Ala	
200 205 210 215	
gaa ttc gat acc gtg gaa gat cta ctt aag cac ttc aat cca gtg tct	785
Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val Ser	
220 225 230	
tgg caa gat gat ctg gag aat ttg tat ctg gac acc cct cat tat aga	833
Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr Arg	
235 240 245	

ggc agg tca tac cat gat cgg aag tcc aaa gtg gac ctg gac agg ctc 881
 Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu
 250 255 260

aat gat gat gtc aag cgt tac agt tgc act ccc agg aat cac tct gtg 929
 Asn Asp Asp Val Lys Arg Tyr Ser Cys Thr Pro Arg Asn His Ser Val
 265 270 275

aac ctc agg gag gag ctg aag ctg acc aat gca gtc ttc ttc cca cga 977
 Asn Leu Arg Glu Glu Leu Lys Leu Thr Asn Ala Val Phe Phe Pro Arg
 280 285 290 295

tgc ctc ctc gtg cag cgc tgt ggt ggc aac tgt ggt tgc gga act gtc 1025
 Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val
 300 305 310

aac tgg aag tcc tgc aca tgc agc tca ggg aag aca gtg aag aag tat 1073
 Asn Trp Lys Ser Cys Thr Cys Ser Ser Gly Lys Thr Val Lys Lys Tyr
 315 320 325

cat gag gta ttg aag ttt gag cct gga cat ttc aag aga agg ggc aaa 1121
 His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly Lys
 330 335 340

gct aag aat atg gct ctt gtt gat atc cag ctg gat cat cat gag cga 1169
 Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg
 345 350 355

tgt gac tgt atc tgc agc tca aga cca cct cga taa aacactatgc 1215
 Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

acatctgtac ttgattatg aaaggacctt taggttacaa aaaccctaag aagcttctaa 1275
 tctcagtga atgaatgcat atggaaatgt tgctttgtta gtgcatggc aagaagaagc 1335
 aaatatcatt aatttctata tacataaaca taggaattca cttatcaata gtatgtgaag 1395
 atatgtatat atacttatat acatgactag ctctatgtat gtaaatagat taaatacttt 1455
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<210> 53

<211> 370

<212> PRT

<213> Mus musculus

<400> 53

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			20					25					30		
Leu	Arg	Asn	Ala	Asn	Leu	Arg	Arg	Asp	Glu	Ser	Asn	His	Leu	Thr	Asp
		35					40					45			
Leu	Tyr	Gln	Arg	Glu	Glu	Asn	Ile	Gln	Val	Thr	Ser	Asn	Gly	His	Val
	50					55					60				
Gln	Ser	Pro	Arg	Phe	Pro	Asn	Ser	Tyr	Pro	Arg	Asn	Leu	Leu	Leu	Thr
65					70					75					80
Trp	Trp	Leu	Arg	Ser	Gln	Glu	Lys	Thr	Arg	Ile	Gln	Leu	Ser	Phe	Asp
			85						90					95	
His	Gln	Phe	Gly	Leu	Glu	Glu	Ala	Glu	Asn	Asp	Ile	Cys	Arg	Tyr	Asp
		100						105					110		
Phe	Val	Glu	Val	Glu	Glu	Val	Ser	Glu	Ser	Ser	Thr	Val	Val	Arg	Gly
	115						120					125			
Arg	Trp	Cys	Gly	His	Lys	Glu	Ile	Pro	Pro	Arg	Ile	Thr	Ser	Arg	Thr
	130					135					140				
Asn	Gln	Ile	Lys	Ile	Thr	Phe	Lys	Ser	Asp	Asp	Tyr	Phe	Val	Ala	Lys
145				150						155					160
Pro	Gly	Phe	Lys	Ile	Tyr	Tyr	Ser	Phe	Val	Glu	Asp	Phe	Gln	Pro	Glu
			165						170					175	
Ala	Ala	Ser	Glu	Thr	Asn	Trp	Glu	Ser	Val	Thr	Ser	Ser	Phe	Ser	Gly
		180					185						190		
Val	Ser	Tyr	His	Ser	Pro	Ser	Ile	Thr	Asp	Pro	Thr	Leu	Thr	Ala	Asp
	195						200					205			
Ala	Leu	Asp	Lys	Thr	Val	Ala	Glu	Phe	Asp	Thr	Val	Glu	Asp	Leu	Leu
	210					215					220				
Lys	His	Phe	Asn	Pro	Val	Ser	Trp	Gln	Asp	Asp	Leu	Glu	Asn	Leu	Tyr
225					230					235					240
Leu	Asp	Thr	Pro	His	Tyr	Arg	Gly	Arg	Ser	Tyr	His	Asp	Arg	Lys	Ser
			245						250					255	
Lys	Val	Asp	Leu	Asp	Arg	Leu	Asn	Asp	Asp	Val	Lys	Arg	Tyr	Ser	Cys
		260						265					270		
Thr	Pro	Arg	Asn	His	Ser	Val	Asn	Leu	Arg	Glu	Glu	Leu	Lys	Leu	Thr
		275					280					285			
Asn	Ala	Val	Phe	Phe	Pro	Arg	Cys	Leu	Leu	Val	Gln	Arg	Cys	Gly	Gly
	290					295					300				
Asn	Cys	Gly	Cys	Gly	Thr	Val	Asn	Trp	Lys	Ser	Cys	Thr	Cys	Ser	Ser
305					310					315					320

[illegible]